



SEQUENCE LISTING

<110> CO, MAN SUNG  
VASQUEZ, MAXIMILIANO  
CARRENO, BEATRIZ  
CELNICKER, ABBIE CHERYL  
COLLINS, MARY  
GOLDMAN, SAMUEL  
GRAY, GARY S.  
KNIGHT, ANDREA  
O'HARA, DENISE  
RUP, BONITA  
VELDMAN, GEERTRUIDA M.

<120> HUMANIZED IMMUNOGLOBULIN REACTIVE WITH B7-2 AND METHODS  
OF TREATMENT THEREWITH

<130> 08702.0081-01000

C 7 <140> 09/627,896  
<141> 2000-07-27

<160> 32

<170> PatentIn Ver. 2.1

<210> 1  
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<220>  
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<222> (1)..(405)  
<223> Anti-B7-2 heavy chain

<400> 1  
atg ggt tgg aac tgt atc atc ttc ttt ctg gtt aca aca gct aca ggt  
48  
Met Gly Trp Asn Cys Ile Ile Phe Phe Leu Val Thr Thr Ala Thr Gly  
1 5 10 15

gtg cac tcc cag gtc cag ctg cag cag tct ggg cct gag ctg gtg agg  
96  
Val His Ser Gln Val Gln Leu Gln Ser Gly Pro Glu Leu Val Arg  
20 25 30

cct ggg gaa tca gtg aag att tcc tgc aag ggt tcc ggc tac aca ttc  
144

Pro Gly Glu Ser Val Lys Ile Ser Cys Lys Gly Ser Gly Tyr Thr Phe  
35 40 45

act gat tat gct ata cag tgg gtg aag cag agt cat gca aag agt cta  
192

Thr Asp Tyr Ala Ile Gln Trp Val Lys Gln Ser His Ala Lys Ser Leu  
50 55 60

gag tgg att gga gtt att aat att tac tat gat aat aca aac tac aac  
240

Glu Trp Ile Gly Val Ile Asn Ile Tyr Tyr Asp Asn Thr Asn Tyr Asn  
65 70 75 80

cag aag ttt aag ggc aag gcc aca atg act gta gac aaa tcc tcc agc  
288

Gln Lys Phe Lys Gly Lys Ala Thr Met Thr Val Asp Lys Ser Ser Ser  
85 90 95

aca gcc tat atg gaa ctt gcc aga ttg aca tct gag gat tct gcc atc  
336

Thr Ala Tyr Met Glu Leu Ala Arg Leu Thr Ser Glu Asp Ser Ala Ile  
100 105 110

tat tac tgt gca aga gcg gcc tgg tat atg gac tac tgg ggt caa gga  
384

Tyr Tyr Cys Ala Arg Ala Ala Trp Tyr Met Asp Tyr Trp Gly Gln Gly  
115 120 125

acc tca gtc acc gtc tcc tca  
405

Thr Ser Val Thr Val Ser Ser  
130 135

<210> 2

<211> 135

<212> PRT

<213> Murine sp.

<220>

<223> Anti-B7-2 heavy chain

<400> 2

Met Gly Trp Asn Cys Ile Ile Phe Phe Leu Val Thr Thr Ala Thr Gly  
1 5 10 15

Val His Ser Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Arg  
20 25 30

Pro Gly Glu Ser Val Lys Ile Ser Cys Lys Gly Ser Gly Tyr Thr Phe  
35 40 45

Thr Asp Tyr Ala Ile Gln Trp Val Lys Gln Ser His Ala Lys Ser Leu  
50 55 60

Glu Trp Ile Gly Val Ile Asn Ile Tyr Tyr Asp Asn Thr Asn Tyr Asn  
65 70 75 80

Gln Lys Phe Lys Gly Lys Ala Thr Met Thr Val Asp Lys Ser Ser Ser  
85 90 95

Thr Ala Tyr Met Glu Leu Ala Arg Leu Thr Ser Glu Asp Ser Ala Ile  
100 105 110

Tyr Tyr Cys Ala Arg Ala Ala Trp Tyr Met Asp Tyr Trp Gly Gln Gly  
115 120 125

Thr Ser Val Thr Val Ser Ser  
130 135

<210> 3  
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<212> DNA  
<213> Murine sp.

<220>  
<221> CDS  
<222> (1)..(396)  
<223> Anti-B7-2 light chain

<400> 3  
atg gat tca cag gcc cag gtt ctt ata ttg ctg ctg cta tgg gta tct  
48  
Met Asp Ser Gln Ala Gln Val Leu Ile Leu Leu Leu Trp Val Ser  
1 5 10 15

ggt acc tgt ggg gac att gtg ctg tca cag tct cca tcc tcc ctg gct  
96

Gly Thr Cys Gly Asp Ile Val Leu Ser Gln Ser Pro Ser Ser Leu Ala  
20 25 30

gtg tca gca gga gag aag gtc act atg agc tgc aaa tcc agt cag agt  
144

Val Ser Ala Gly Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser  
35 40 45

ctg ctc aac agt aga acc cga gag aac tac ttg gct tgg tac cag cag  
192

Leu Leu Asn Ser Arg Thr Arg Glu Asn Tyr Leu Ala Trp Tyr Gln Gln  
50 55 60

aaa cca ggg cag tct cct aaa ctg ctg atc tac tgg gca tcc act agg  
240

Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg  
65 70 75 80

gaa tct ggg gtc cct gat cgc ttc aca ggc agt gga tct ggg aca gat  
288

Glu Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp  
85 90 95

ttc act ctc acc atc agc agt gtg cag gct gaa gac ctg gca gtt tat  
336

Phe Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr  
100 105 110

tac tgc acg caa tct tat aat ctt tac acg ttc gga ggg ggg acc aag  
384

Tyr Cys Thr Gln Ser Tyr Asn Leu Tyr Thr Phe Gly Gly Gly Thr Lys  
115 120 125

ctg gaa ata aaa  
396

Leu Glu Ile Lys  
130

<210> 4

<211> 132

<212> PRT

<213> Murine sp.

<220>

<223> Anti-B7-2 light chain

<400> 4

Met Asp Ser Gln Ala Gln Val Leu Ile Leu Leu Leu Trp Val Ser  
1 5 10 15

Gly Thr Cys Gly Asp Ile Val Leu Ser Gln Ser Pro Ser Ser Leu Ala  
20 25 30

Val Ser Ala Gly Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser  
35 40 45

Leu Leu Asn Ser Arg Thr Arg Glu Asn Tyr Leu Ala Trp Tyr Gln Gln  
50 55 60

Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg  
65 70 75 80

Glu Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp  
85 90 95

Phe Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr  
100 105 110

Tyr Cys Thr Gln Ser Tyr Asn Leu Tyr Thr Phe Gly Gly Gly Thr Lys  
115 120 125

Leu Glu Ile Lys  
130

<210> 5

<211> 405

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Humanized  
murine anti-human B7-2 heavy chain

<220>

<221> CDS

<222> (1)..(405)

<400> 5

atg ggt tgg aac tgt atc atc ttc ttt ctg gtt acc aca gct aca ggt  
48  
Met Gly Trp Asn Cys Ile Ile Phe Phe Leu Val Thr Thr Ala Thr Gly  
1 5 10 15

gtg cac tcc cag gtc cag ctg gtg cag tct ggg gct gag gtg aag aag  
96  
Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys  
20 25 30

cct ggg agc tca gtg aag gtg tcc tgc aaa gct tcc ggc tac aca ttc  
144  
Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe  
35 40 45

act gat tat gct ata cag tgg gtg aga cag gct cct gga cag ggc ctc  
192  
Thr Asp Tyr Ala Ile Gln Trp Val Arg Gln Ala Pro Gly Gln Gly Leu  
50 55 60

gag tgg att gga gtt att aat att tac tat gat aat aca aac tac aac  
240  
Glu Trp Ile Gly Val Ile Asn Ile Tyr Tyr Asp Asn Thr Asn Tyr Asn  
65 70 75 80

cag aag ttt aag ggc aag gcc aca atg act gta gac aag tcg acg agc  
288  
Gln Lys Phe Lys Gly Lys Ala Thr Met Thr Val Asp Lys Ser Thr Ser  
85 90 95

aca gcc tat atg gaa ctt agt tct ttg aga tct gag gat acg gcc gtt  
336  
Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val  
100 105 110

tat tac tgt gca aga gcg gcc tgg tat atg gac tac tgg ggt caa ggt  
384  
Tyr Tyr Cys Ala Arg Ala Ala Trp Tyr Met Asp Tyr Trp Gly Gln Gly  
115 120 125

acc ctt gtc acc gtc tcc tca  
405  
Thr Leu Val Thr Val Ser Ser  
130 135

<211> 135

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Humanized  
murine anti-human B7-2 heavy chain

<400> 6

Met Gly Trp Asn Cys Ile Ile Phe Phe Leu Val Thr Thr Ala Thr Gly  
1 5 10 15

Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys  
20 25 30

Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe  
35 40 45

Thr Asp Tyr Ala Ile Gln Trp Val Arg Gln Ala Pro Gly Gln Gly Leu  
50 55 60

Glu Trp Ile Gly Val Ile Asn Ile Tyr Tyr Asp Asn Thr Asn Tyr Asn  
65 70 75 80

Gln Lys Phe Lys Gly Lys Ala Thr Met Thr Val Asp Lys Ser Thr Ser  
85 90 95

Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val  
100 105 110

Tyr Tyr Cys Ala Arg Ala Ala Trp Tyr Met Asp Tyr Trp Gly Gln Gly  
115 120 125

Thr Leu Val Thr Val Ser Ser  
130 135

<210> 7

<211> 396

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Humanized  
murine anti-human B7-2 light chain

<220>

<221> CDS

<222> (1)..(396)

<400> 7

atg gat tca cag gcc cag gtt ctt ata ttg ctg ctg cta tgg gta tct  
48

Met Asp Ser Gln Ala Gln Val Leu Ile Leu Leu Leu Leu Trp Val Ser  
1 5 10 15

ggc acc tgt ggg gac att gtg ctg aca cag tct cca gat tcc ctg gct  
96

Gly Thr Cys Gly Asp Ile Val Leu Thr Gln Ser Pro Asp Ser Leu Ala  
20 25 30

gta agc tta gga gag agg gcc act att agc tgc aaa tcc agt cag agt  
144

Val Ser Leu Gly Glu Arg Ala Thr Ile Ser Cys Lys Ser Ser Gln Ser  
35 40 45

ctg ctc aac agt aga acc cga gag aac tac ttg gct tgg tac cag cag  
192

Leu Leu Asn Ser Arg Thr Arg Glu Asn Tyr Leu Ala Trp Tyr Gln Gln  
50 55 60

aaa cca ggg cag cct cct aaa ctg ctg atc tac tgg gca tcc act agg  
240

Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg  
65 70 75 80

gaa tct ggg gtc cct gat cgc ttc agt ggc agt gga tct ggg aca gat  
288

Glu Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Thr Asp  
85 90 95

ttc act ctc acc atc agc agt ctg cag gct gaa gac gtg gca gtt tat  
336

Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr  
100 105 110

tac tgc acg caa tct tat aat ctt tac acg ttc gga cag ggg acc aag  
384

Tyr Cys Thr Gln Ser Tyr Asn Leu Tyr Thr Phe Gly Gln Gly Thr Lys  
115 120 125

gtg gaa ata aaa

396

Val Glu Ile Lys

130

<210> 8

<211> 132

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Humanized  
murine anti-human B7-2 light chain

<400> 8

Met Asp Ser Gln Ala Gln Val Leu Ile Leu Leu Leu Trp Val Ser  
1 5 10 15

Gly Thr Cys Gly Asp Ile Val Leu Thr Gln Ser Pro Asp Ser Leu Ala  
20 25 30

Val Ser Leu Gly Glu Arg Ala Thr Ile Ser Cys Lys Ser Ser Gln Ser  
35 40 45

Leu Leu Asn Ser Arg Thr Arg Glu Asn Tyr Leu Ala Trp Tyr Gln Gln  
50 55 60

Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg  
65 70 75 80

Glu Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Thr Asp  
85 90 95

Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr  
100 105 110

Tyr Cys Thr Gln Ser Tyr Asn Leu Tyr Thr Phe Gly Gln Gly Thr Lys  
115 120 125

Val Glu Ile Lys

130

<210> 9

<211> 15

<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: CDR1 of  
humanized murine anti-human B7-2 heavy chain

<220>  
<221> CDS  
<222> (1)..(15)

<400> 9  
gat tat gct ata cag  
15  
Asp Tyr Ala Ile Gln  
1 5

<210> 10  
<211> 5  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: CDR1 of humanized  
murine anti-human B7-2 heavy chain

<400> 10  
Asp Tyr Ala Ile Gln  
1 5

<210> 11  
<211> 51  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: CDR2 of  
humanized murine anti-human B7-2 heavy chain

<220>  
<221> CDS  
<222> (1)..(51)

<400> 11

gtt att aat att tac tat gat aat aca aac tac aac cag aag ttt aag  
48

Val Ile Asn Ile Tyr Tyr Asp Asn Thr Asn Tyr Asn Gln Lys Phe Lys  
1 5 10 15

ggc

51

Gly

<210> 12

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: CDR2 of humanized  
murine anti-human B7-2 heavy chain

<400> 12

Val Ile Asn Ile Tyr Tyr Asp Asn Thr Asn Tyr Asn Gln Lys Phe Lys  
1 5 10 15

Gly

<210> 13

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: CDR3 of  
humanized murine anti-human B7-2 heavy chain

<220>

<221> CDS

<222> (1)..(21)

<400> 13

gct gcc tgg tat atg gac tac

21

Ala Ala Trp Tyr Met Asp Tyr

1 5

<210> 14

<211> 7  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: CDR3 of humanized murine anti-human B7-2 heavy chain

<400> 14  
Ala Ala Trp Tyr Met Asp Tyr  
1 5

<210> 15  
<211> 51  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: CDR1 of humanized murine anti-human B7-2 light chain

<220>  
<221> CDS  
<222> (1)..(51)

<400> 15  
aaa tcc agt cag agt ctg ctc aac agt aga acc cga gag aac tac ttg  
48  
Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Arg Glu Asn Tyr Leu  
1 5 10 15

gct  
51  
Ala

<210> 16  
<211> 17  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: CDR1 of humanized murine anti-human B7-2 light chain

<400> 16

Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Arg Glu Asn Tyr Leu  
1 5 10 15

Ala

<210> 17  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: CDR2 of  
humanized murine anti-human B7-2 light chain

<220>  
<221> CDS  
<222> (1)..(21)

<400> 17  
tgg gca tcc act agg gaa tct  
21  
Trp Ala Ser Thr Arg Glu Ser  
1 5

<210> 18  
<211> 7  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: CDR2 of humanized  
murine anti-human B7-2 light chain

<400> 18  
Trp Ala Ser Thr Arg Glu Ser  
1 5

<210> 19  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: CDR3 of

humanized murine anti-human B7-2 light chain

<220>  
<221> CDS  
<222> (1)..(24)

<400> 19  
acg caa tct tat aat ctt tac acg  
24  
Thr Gln Ser Tyr Asn Leu Tyr Thr  
1 5

<210> 20  
<211> 8  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: CDR3 of humanized  
murine anti-human B7-2 light chain

<400> 20  
Thr Gln Ser Tyr Asn Leu Tyr Thr  
1 5

<210> 21  
<211> 1960  
<212> DNA  
<213> Mus sp.

<220>  
<221> CDS  
<222> (12)..(408)

<220>  
<221> CDS  
<222> (768)..(1087)  
<223> 3D1 light chain

<400> 21  
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50  
Met Asp Ser Gln Ala Gln Val Leu Ile Leu Leu Leu  
1 5 10

tgg gta tct ggc acc tgt ggg gac att gtg ctg aca cag tct cca gat  
98

Trp Val Ser Gly Thr Cys Gly Asp Ile Val Leu Thr Gln Ser Pro Asp  
15 20 25

tcc ctg gct gta agc tta gga gag agg gcc act att agc tgc aaa tcc  
146

Ser Leu Ala Val Ser Leu Gly Glu Arg Ala Thr Ile Ser Cys Lys Ser  
30 35 40 45

agt cag agt ctg ctc aac agt aga acc cga gag aac tac ttg gct tgg  
194

Ser Gln Ser Leu Leu Asn Ser Arg Thr Arg Glu Asn Tyr Leu Ala Trp  
50 55 60

tac cag cag aaa cca ggg cag cct cct aaa ctg ctg atc tac tgg gca  
242

Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp Ala  
65 70 75

tcc act agg gaa tct ggg gtc cct gat cgc ttc agt ggc agt gga tct  
290

Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser  
80 85 90

ggg aca gat ttc act ctc acc atc agc agt ctg cag gct gaa gac gtg  
338

Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp Val  
95 100 105

gca gtt tat tac tgc agc caa tct tat aat ctt tac acg ttc gga cag  
386

Ala Val Tyr Tyr Cys Ser Gln Ser Tyr Asn Leu Tyr Thr Phe Gly Gln  
110 115 120 125

ggg acc aag gtg gaa ata aaa c gtaagtagtc ttctcaactc tagaaattct  
438

Gly Thr Lys Val Glu Ile Lys  
130

aaactctgag ggggtcgat gacgtggcca ttcttcgcct aaagcattga gtttactgca  
498

aggcagaaa agcatgcaaa gccctcagaa tggctgcaaa gagctccaac aaaacaattt  
558

agaactttat taaggaatag gggaaagcta ggaagaaact caaaacatca agatttaaa  
618

tacgcttctt ggtctccttg ctataattat ctgggataag catgctgttt tctgtctgtc  
678

cctaacatgc cctgtgatta tccgcaaaca acacacccaa gggcagaact ttgttactta  
738

aacaccatcc tggggcttc tttcctcag ga act gtg gct gca cca tct gtc  
790

Arg Thr Val Ala Ala Pro Ser Val  
135 140

ttc atc ttc ccg cca tct gat gag cag ttg aaa tct gga act gcc tct  
838

Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser  
145 150 155

gtt gtg tgc ctg ctg aat aac ttc tat ccc aga gag gcc aaa gta cag  
886

Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln  
160 165 170

tgg aag gtg gat aac gcc ctc caa tcg ggt aac tcc cag gag agt gtc  
934

Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val  
175 180 185

aca gag cag gac agc aag gac agc acc tac agc ctc agc agc acc ctg  
982

Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu  
190 195 200

acg ctg agc aaa gca gac tac gag aaa cac aaa gtc tac gcc tgc gaa  
1030

Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu  
205 210 215 220

gtc acc cat cag ggc ctg agc tcg ccc gtc aca aag agc ttc aac agg  
1078

Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg  
225 230 235

gga gag tgt tagagggaga agtgccccc cctgctcctc agttccagcc  
1127

Gly Glu Cys

tgacccctc ccatccttg gcctctgacc cttttccac aggggaccta cccctattgc  
1187

ggtcctccag ctcatcttc acctcacccc ctcctcctc cttggctta attatgctaa  
1247

tgtggagga gaatgaataa ataaagtcaa tctttgcacc tgtggttct ctcttcctc  
1307

attnataat tattatctgt tgtttacca actactcaat ttcttataa agggactaaa  
1367

tatgttagtca tcctaaggcg cataaccatt tataaaaatc atccttcatt ctatttacc  
1427

ctatcatcct ctgcaagaca gtcctccctc aaaccacaa gccttctgtc ctcacagtcc  
1487

cctggccat ggttaggagag acttgcttcc ttgtttccc ctctcagca agccctcata  
1547

gtcctttta agggtgacag gtcttacagt catatatcct ttgattcaat tccctggaa  
1607

tcaaccaaag caaatttttc aaaagaagaa acctgctata aagagaatca ttcattgcaa  
1667

catgatataa aataacaaca caataaaagc aattaaataa acaaacaata gggaaatgtt  
1727

taagttcatc atggtactta gacttaatgg aatgtcatgc ctttattaca tttttaaaca  
1787

ggtaactgagg gactcctgtc tgccaaggc cgtattgagt actttccaca acctaattta  
1847

atccacacta tactgtgaga taaaaacat tcattaaat gttgcaaagg ttctataaag  
1907

ctgagagaca aatatattct ataactcagc aatcccactt ctaggatcaa ttc  
1960

<210> 22

<211> 239

<212> PRT

<213> Mus sp.

<223> 3D1 light chain

<400> 22

Met Asp Ser Gln Ala Gln Val Leu Ile Leu Leu Leu Trp Val Ser  
1 5 10 15

Gly Thr Cys Gly Asp Ile Val Leu Thr Gln Ser Pro Asp Ser Leu Ala  
20 25 30

Val Ser Leu Gly Glu Arg Ala Thr Ile Ser Cys Lys Ser Ser Gln Ser  
35 40 45

Leu Leu Asn Ser Arg Thr Arg Glu Asn Tyr Leu Ala Trp Tyr Gln Gln  
50 55 60

Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg  
65 70 75 80

Glu Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp  
85 90 95

Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr  
100 105 110

Tyr Cys Ser Gln Ser Tyr Asn Leu Tyr Thr Phe Gly Gln Gly Thr Lys  
115 120 125

Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro  
130 135 140

Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu  
145 150 155 160

Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp  
165 170 175

Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp  
180 185 190

Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys  
195 200 205

Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln  
210 215 220

Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
225 230 235

<210> 23  
<211> 2249  
<212> DNA  
<213> 3D1 heavy chain

<220>  
<221> CDS  
<222> (12) .. (417)

<220>  
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<220>  
<221> CDS  
<222> (1495) .. (1821)

<220>  
<221> CDS  
<222> (1919) .. (2238)

<400> 23  
tctagaccac c atg ggt tgg aac tgt atc atc ttc ttt ctg gtt acc aca  
50

Met Gly Trp Asn Cys Ile Ile Phe Phe Leu Val Thr Thr  
1 5 10

gct aca ggt gtg cac tcc cag gtc cag ctg gtg cag tct ggg gct gag  
98

Ala Thr Gly Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu  
15 20 25

gtg aag aag cct ggg agc tca gtg aag gtg tcc tgc aaa gct tcc ggc  
146

Val Lys Lys Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly  
30 35 40 45

tac aca ttc act gat tat gct ata cag tgg gtg aga cag gct cct gga  
194

Tyr Thr Phe Thr Asp Tyr Ala Ile Gln Trp Val Arg Gln Ala Pro Gly  
50 55 60

cag ggc ctc gag tgg att gga gtt att aat att tac tat gat aat aca  
242

Gln Gly Leu Glu Trp Ile Gly Val Ile Asn Ile Tyr Tyr Asp Asn Thr  
65 70 75

aac tac aac cag aag ttt aag ggc aag gcc aca atg act gta gac aag  
290

Asn Tyr Asn Gln Lys Phe Lys Gly Lys Ala Thr Met Thr Val Asp Lys  
80 85 90

tcg acg agc aca gcc tat atg gaa ctt agt tct ttg aga tct gag gat  
338

Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp  
95 100 105

acg gcc gtt tat tac tgt gca aga gcg gcc tgg tat atg gac tac tgg  
386

Thr Ala Val Tyr Tyr Cys Ala Arg Ala Ala Trp Tyr Met Asp Tyr Trp  
110 115 120 125

ggt caa ggt acc ctt gtc acc gtc tcc tca g gtgagtcctt aaaacctcta  
437

Gly Gln Gly Thr Leu Val Thr Val Ser Ser  
130 135

gagcttctg gggcgagccg ggcctgactt tggcttggg gcagggagtg ggctaaggta  
497

aggcaggtgg cgccagccag gtgcacaccc aatgcccgtg agcccagaca ctggaccctg  
557

cctggaccct cgtggataga caagaaccga ggggcctctg cgccctggc ccagctctgt  
617

cccacaccgc ggtcacatgg caccacctct cttgcag cc tcc acc aag ggc cca  
671

Ala Ser Thr Lys Gly Pro  
140

tcg gtc ttc ccc ctg gcg ccc tgc tcc agg agc acc tcc gag agc aca  
719

Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr  
145 150 155

gcg gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccg gtg acg  
767

Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr  
160 165 170

gtg tcg tgg aac tca ggc gct ctg acc agc ggc gtg cac acc ttc cca  
815

Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro  
175 180 185

gct gtc cta cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc  
863

Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr  
190 195 200 205

gtg ccc tcc agc aac ttc ggc acc cag acc tac acc tgc aac gta gat  
911

Val Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp  
210 215 220

cac aag ccc agc aac acc aag gtg gac aag aca gtt g gtgagaggcc  
958

His Lys Pro Ser Asn Thr Lys Val Asp Lys Thr Val  
225 230

agctcaggga gggagggtgt ctgcttggaaag ccaggctcag ccctcctgcc tggacgcacc  
1018

ccggctgtgc agccccagcc cagggcagca aggcaggccc catctgtctc ctcacccgga  
1078

ggctctgcc cgccccactc atgctcaggag agagggtctt ctggctttt ccaccaggct  
1138

ccaggcaggc acaggctggg tgcccctacc ccaggccctt cacacacagg ggcaggtgct  
1198

tggctcagac ctgccaaaag ccatatccgg gaggaccctg cccctgaccc aagccgaccc  
1258

caaaggccaa actgtccact ccctcagctc ggacacccctc tctcctccca gatccgagta  
1318

actcccaatc ttctctctgc ag ag cgc aaa tgt tgt gtc gag tgc cca ccg  
1369

Glu Arg Lys Cys Cys Val Glu Cys Pro Pro  
235 240

tgc cca g gtaagccagc ccaggcctcg ccctccagct caaggcgaaa caggtgccct  
1426

Cys Pro  
245

agagttagcct gcatccaggg acaggcccc a gctgggtgct gacacgtcca cctccatctc  
1486

ttcctcg ca cca cct gcg gca gca ccg tca gtc ttc ctc ttc ccc cca  
1535

Ala Pro Pro Ala Ala Ala Pro Ser Val Phe Leu Phe Pro Pro  
250 255

aaa ccc aag gac acc ctc atg atc tcc cgg acc cct gag gtc acg tgc  
1583

Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys
260					265					270					275

gtg gtg gtg gac gtg agc cac gaa gac ccc gag gtc cag ttc aac tgg  
1631

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Gln Phe Asn Trp  
280 285 290

tac gtg gac ggc gtg gag gtg cat aat gcc aag aca aag cca cgg gag  
1679

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu  
 295 300 305

gag cag ttc aac agc acg ttc cgt gtg gtc agc gtc ctc acc gtt gtg  
1727

Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Val  
 310 315 320

cac cag gac tgg ctg aac ggc aag gag tac aag tgc aag gtc tcc aac  
1775

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn  
 325 330 335

aaa ggc ctc cca gcc ccc atc gag aaa acc atc tcc aaa acc aaa g  
1821

Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys  
340 345 350

gtgggacccg cgggttatga gggccacatg gacagaggcc ggctcgccccc accctctgcc  
1881

ctgggagtga ccgctgtgcc aacctctgtc cctacag gg cag ccc cga gaa cca  
1935

Gly Gln Pro Arg Glu Pro  
355 360

cag gtg tac acc ctg ccc cca tcc cgg gag gag atg acc aag aac cag  
1983

Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln  
365 370 375

gtc agc ctg acc tgc ctg gtc aaa ggc ttc tac ccc agc gac atc gcc  
2031

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala  
380 385 390

gtg gag tgg gag agc aat ggg cag ccg gag aac aac tac aag acc aca  
2079

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Thr Lys Thr  
395 400 405

cct ccc atg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc  
2127

Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu  
410 415 420

acc gtg gac aag agc agg tgg cag cag ggg aac gtc ttc tca tgc tcc  
2175

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser  
425 430 435 440

gtg atg cat gag gct ctg cac aac cac tac acg cag aag agc ctc tcc  
2223

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser  
445 450 455

ctg tcc ccg ggt aaa tgagtgaatt c  
2249  
Leu Ser Pro Gly Lys  
460

<210> 24  
<211> 462  
<212> PRT  
<213> 3D1 heavy chain  
  
<400> 24

Met Gly Trp Asn Cys Ile Ile Phe Phe Leu Val Thr Thr Ala Thr Gly  
1 5 10 15

Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys  
20 25 30

Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe  
35 40 45

Thr Asp Tyr Ala Ile Gln Trp Val Arg Gln Ala Pro Gly Gln Gly Leu  
50 55 60

Glu Trp Ile Gly Val Ile Asn Ile Tyr Tyr Asp Asn Thr Asn Tyr Asn  
65 70 75 80

Gln Lys Phe Lys Gly Lys Ala Thr Met Thr Val Asp Lys Ser Thr Ser  
85 90 95

Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val  
100 105 110

Tyr Tyr Cys Ala Arg Ala Ala Trp Tyr Met Asp Tyr Trp Gly Gln Gly  
115 120 125

Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe  
130 135 140

Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu  
145 150 155 160

Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp  
165 170 175

Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu  
180 185 190

Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser  
195 200 205

Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp His Lys Pro  
210 215 220

Ser Asn Thr Lys Lys Val Asp Lys Thr Val Glu Arg Lys Cys Cys Val  
225 230 235 240

Glu Cys Pro Pro Cys Pro Ala Pro Pro Ala Ala Ala Pro Ser Val Phe  
245 250 255

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro  
260 265 270

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val  
275 280 285

Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr  
290 295 300

Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser Val  
305 310 315 320

Leu Thr Val Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys  
325 330 335

Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser  
340 345 350

Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro  
355 360 365

Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val  
370 375 380

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly  
385 390 395 400

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser Asp  
405 410 415

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp  
420 425 430

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His  
435 440 445

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys  
450 455 460

<210> 25  
<211> 327  
<212> DNA  
<213> Homo sapiens  
<223> III2R light chain variable region

<400> 25  
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60

atcacttgcc gggcgagtca gggcattagc aattatttag cctggtatca gcagaaacca  
120

gggaaagtgc ctaagctcct gatctatgct gcatccactt tgcaatcagg ggtcccatct  
180

cggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag cctgcagcct  
240

gaagatgttgc caacttatta ctgtcaaaag tataacagtg cccctccgag tacgttcggc  
300

caagggacca aggtggaaat caaacgt  
327

<210> 26

<211> 339

<212> DNA

<213> Homo sapiens

<223> H2F light chain variable region

<400> 26

gacatccagt tgacccagtc tccagactcc ctggctgtgt ctctggcga gagggccacc  
60

atcaactgca agtccagcca gagtgttta tacagctcca acaacaagaa ttacttaact  
120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactggc atctaccgg  
180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagattt cactctcacc  
240

atcagcagcc tgcaggctga agatgtggca gtttattact gtcagcaata ttatagtact  
300

cctcgaacgt tcggccaagg gaccaaggtg gaaatcaaa  
339

<210> 27

<211> 95

<212> PRT

<213> Homo sapiens

<223> III2R light chain variable region

<400> 27

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly  
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Asn Tyr  
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Val Pro Lys Leu Leu Ile  
35 40 45

Tyr Ala Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly  
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro  
65 70 75 80

Glu Asp Val Ala Thr Tyr Tyr Cys Gln Lys Tyr Asn Ser Ala Pro  
85 90 95

<210> 28

<211> 101

<212> PRT

<213> Homo sapiens

<223> H2F light chain variable region

<400> 28

Asp Ile Gln Leu Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly  
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser  
20 25 30

Ser Asn Asn Lys Tyr Leu Thr Trp Tyr Gln Gln Lys Pro Gly Gln Pro  
35 40 45

Pro Lys Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val  
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr  
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln  
85 90 95

Tyr Tyr Ser Thr Pro

100

<210> 29  
<211> 368  
<212> DNA  
<213> Homo sapiens  
<223> III2R heavy chain variable region

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60  
  
cctgcaaggc ttctggaggc accttcagta gttatactat cagctgggtg cgacaggccc  
120  
  
ctggacaagg gcttgagtgg atgggaagga tcatgcctat cttggacta gcaaattacg  
180  
  
cacagaagtt ccagggcaga gtcacgatta ccgcggacaa atccacgagc acagcctaca  
240  
  
tggagctgag cagcctgaga tctgaggaca cggccgtgta ttactgtgcg agagatcccg  
300  
  
attatgttg ggggagcgac aactggttcg acccctgggg ccagggaaacc ctgctcatcg  
360  
  
tctcctca  
368

<210> 30  
<211> 358  
<212> DNA  
<213> Homo sapiens  
<223> H2F heavy chain variable region

<400> 30  
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60  
  
tgtgcagcct cggattcacc tttacttagga atcctacgag ctgggtacgc caggctccag  
120  
  
ggaaggggot ggagtgggtg gttaatataa tggttagtcgg aattgaacca tactatgcgg  
180

actctgtgaa gggccgattc accatctcca gaggcaacgc caagaactca ctgtatctgc  
240

aatgaacag cctgagagcc gaggacacgg ccgtgtatta ctgtgcgaga gggatctgca  
300

ttatgacaga ggctactttg actactgggg ccagggaaacc ctggtcaccg tctcctca  
358

<210> 31

<211> 97

<212> PRT

<213> Homo sapiens

<223> III2R heavy chain variable region

<400> 31

Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser Ser  
1 5 10 15

Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr Thr  
20 25 30

Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly  
35 40 45

Arg Ile Met Pro Ile Leu Gly Leu Ala Asn Tyr Ala Gln Lys Phe Gln  
50 55 60

Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr Met  
65 70 75 80

Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala  
85 90 95

Arg

<210> 32  
<211> 98  
<212> PRT  
<213> Homo sapiens  
<223> H2F heavy chain variable region

<400> 32

Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly Ser  
1 5 10 15

Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr Tyr  
20 25 30

Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser  
35 40 45

Tyr Ile Ser Ser Arg Gly Ser Glu Thr Ile Tyr Tyr Ala Asp Ser Val  
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr  
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

Ala Arg